



SEQUENCE LISTING

<110> Anderson, Annaliesa S.
 Jansen, Kathrin Ute
 Kelly, Rosemarie
 Schultz, Loren D.
 Montgomery, Donna L.
 McClements, William L.

<120> POLYPEPTIDES FOR INDUCING A PROTECTIVE
 IMMUNE RESPONSE AGAINST STAPHYLOCOCCUS AUREUS

<130> 21569YP

<140> US 10/564,458

<141> 2006-01-12

<150> PCT/2004/023523

<151> 2004-07-22

<150> 60/489,840

<151> 2003-07-24

<150> 60/520,115

<151> 2003-11-14

<160> 109

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nI with amino terminus methionine

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Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala
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Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala
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Pro	Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn
65					70				75					80	
Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro
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Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp
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Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	
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Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	
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Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	
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Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	
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Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	
			180					185					190			
Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	
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Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	
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Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	
225					230					235					240	
Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	
			245						250					255		
Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	
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Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	
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Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	
	290				295						300					
Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	
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Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	
			325						330					335		
Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	
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Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	
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Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	
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Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	
385					390					395					400	
Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	
			405						410					415		
Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	
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Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro			
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Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	Ala	Val	Ala	Ser	Pro	Thr	Thr
	50					55					60				
Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser
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Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala
				85					90					95	
Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr	Lys	Glu	Val	Lys
			100					105					110		
Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu
		115					120					125			
Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser
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Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly
145					150					155					160
Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val
				165					170					175	
Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly
			180					185					190		
Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro
		195					200					205			
Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg
	210					215					220				
Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr
225					230					235					240
His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe
				245					250					255	
Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp
			260					265					270		
Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu
		275					280					285			
Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu
	290					295					300				
Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala
305					310					315					320
Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln
				325					330					335	
Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val
			340					345					350		
Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys
		355					360					365			
His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met
		370				375					380				
Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln
385					390					395					400
Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile
				405					410					415	
Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys
			420					425					430		
Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile
		435					440					445			
Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys
	450					455					460				

Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	
465					470					475					480	
Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	
				485					490						495	
Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	
			500					505					510			
Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys	
		515					520					525				
Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	
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Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	
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Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	
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Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	
			580					585					590			
His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	
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Ser	Leu	Pro	Gln	Thr	Gly	Glu	Glu	Ser	Asn	Lys	Asp	Met	Thr	Leu	Pro	
	610					615					620					
Leu	Met	Ala	Leu	Leu	Ala	Leu	Ser	Ser	Ile	Val	Ala	Phe	Val	Leu	Pro	
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<211> 569

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH with amino terminus methionine

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Glu	Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	
			20					25					30			
Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	
		35				40						45				
Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	
	50				55						60					
Pro	Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	
65				70					75						80	
Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	
			85					90					95			
Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	
			100					105					110			
Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	
		115					120					125				
Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	
	130					135					140					
Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	
145					150					155					160	

Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	
				165					170					175		
Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	
			180					185					190			
Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	
		195					200					205				
Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	
	210					215					220					
Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	
225					230					235					240	
Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	
				245					250					255		
Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	
			260					265					270			
Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	
		275					280					285				
Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	
	290					295					300					
Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	
305					310					315					320	
Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	
				325					330					335		
Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	
			340					345					350			
Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	
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Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	
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Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	
385					390					395					400	
Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	
				405					410					415		
Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	
			420					425					430			
Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	
		435					440					445				
Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	
	450					455					460					
Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	
465					470					475					480	
Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	
				485					490					495		
Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	
			500					505					510			
Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	
		515					520					525				
Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	
	530					535					540					
Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	
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Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser								
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH with amino terminus methionine-glycine

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 Thr Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu
 35 40 45
 Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys
 50 55 60
 Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn
 65 70 75 80
 Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn
 85 90 95
 Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile
 100 105 110
 Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr
 115 120 125
 Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro
 130 135 140
 Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu
 145 150 155 160
 Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp
 165 170 175
 Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr
 180 185 190
 Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu
 195 200 205
 Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser
 210 215 220
 Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu
 225 230 235 240
 Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu
 245 250 255
 Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys
 260 265 270
 Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser
 275 280 285
 Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr
 290 295 300
 Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn
 305 310 315 320
 Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met
 325 330 335
 Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr
 340 345 350
 Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys
 355 360 365

Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly
370						375				380					
Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp
385					390					395					400
Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr
				405					410					415	
Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser
			420					425					430		
Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser
		435					440					445			
Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn
		450				455					460				
Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser
465					470					475					480
Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu
				485					490					495	
Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val
			500					505					510		
Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln
		515					520					525			
Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys
		530				535					540				
Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn
545					550					555					560
Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser						
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<210> 5

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH with amino terminus methionine-glycine

<400> 5

Met	Gly	Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys
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Thr	Glu	Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu
			20					25					30		
Thr	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu
		35					40					45			
Ala	Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys
	50					55					60				
Ala	Pro	Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn
65					70					75					80
Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn
				85					90					95	
Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile
			100					105					110		
Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr
		115					120					125			
Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro
						135					140				

Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu
145					150					155					160
Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp
				165					170						175
Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr
			180					185					190		
Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu
		195					200					205			
Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser
	210					215					220				
Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu
225					230					235					240
Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu
				245					250					255	
Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys
			260					265					270		
Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser
		275					280					285			
Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr
	290					295					300				
Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn
305					310					315					320
Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met
				325					330					335	
Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr
			340					345					350		
Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys
		355					360					365			
Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly
	370					375					380				
Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp
385					390					395					400
Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr
				405					410					415	
Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser
			420					425					430		
Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	
		435					440					445			

<210> 6

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 6

Ala	Glu	Glu	Thr	Gly	Val	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala
			20					25					30		
Lys	Pro	Val	Ala	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys
		35					40					45			

Glu	Val	Val	Ala	Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys
50						55					60				
Ala	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Ala	Lys	Glu	Glu	Lys	Pro
65					70					75					80
Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu
				85					90				95		
Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala
			100					105					110		
Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr
		115					120					125			
Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile
	130					135					140				
Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln
145					150					155					160
Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile
				165					170					175	
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe
			180					185					190		
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His
		195					200					205			
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala
	210					215					220				
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr
225					230					235					240
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu
				245					250					255	
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys
			260					265					270		
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu
		275					280					285			
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro
	290					295					300				
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr
305					310					315					320
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Ala	Phe	Val	Lys	His
				325					330					335	
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu
			340					345					350		
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg
		355					360					365			
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile
	370					375					380				
Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val
385					390					395					400
His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val
			405						410					415	
Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Ala	Asp	Lys	Thr	Asn	Lys	Lys
			420					425					430		
Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Thr	Thr	Pro	Ala	Met	Pro
		435					440					445			
Ser	Lys	Pro	Thr	Thr	Pro	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp
	450					455					460				
Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Ser	Pro	Ser	Val	Glu	Lys	Glu	Asn
465					470					475					480

Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Met	Pro	Val	Thr	Lys	Pro
				485					490					495	
Ala	Lys	Ala	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val
			500					505					510		
Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Glu	Thr
		515					520					525			
Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp
	530					535					540				
Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His
545					550					555					560
Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser
				565					570					575	

<210> 7

<211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 7

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
		35					40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50					55					60				
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr
65				70					75						80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
			85						90				95		
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
		100						105					110		
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
		115					120					125			
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
	130					135					140				
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145				150						155					160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
			165						170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
		180						185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195					200					205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225				230						235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	

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Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
      260      265      270
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
      275      280      285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
      290      295      300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
      305      310      315      320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
      325      330      335
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
      340      345      350
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
      355      360      365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
      370      375      380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
      385      390      395      400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
      405      410      415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
      420      425      430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
      435      440      445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
      450      455      460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
      465      470      475      480
Gly Val Thr Leu Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
      485      490      495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
      500      505      510
Pro Thr Thr Gly Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
      515      520      525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
      530      535      540
Ile Lys His Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
      545      550      555      560
Thr Gln Glu Asn Lys Ala Lys Ser
      565

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<210> 8

<211> 568

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 8

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Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
  1      5      10      15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
      20      25      30

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Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
		35					40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50					55					60				
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr
65				70						75					80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
				85				90					95		
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
			100					105					110		
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
		115					120					125			
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
	130					135					140				
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145				150						155					160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
				165					170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195					200					205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225				230						235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275					280					285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305				310						315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325				330						335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385				390						395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
				405				410						415	
Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		
Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val
		435					440					445			
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
	450					455					460				

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Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465          470          475          480
Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
          485          490          495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
          500          505          510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
          515          520          525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
          530          535          540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545          550          555          560
Thr Gln Glu Asn Lys Ala Lys Ser
          565

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<210> 9
<211> 568
<212> PRT
<213> Artificial Sequence

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<220>
<223> ORF0657nH

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<400> 9
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1      5      10      15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
          20      25      30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
          35      40      45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
          50      55      60
Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
65      70      75      80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
          85      90      95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
          100     105     110
Glu Met Lys Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser
          115     120     125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
          130     135     140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145     150     155     160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
          165     170     175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
          180     185     190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
          195     200     205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
210     215     220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
225     230     235     240

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Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
 245 250 255
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
 260 265 270
 Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
 275 280 285
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
 290 295 300
 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
 305 310 315 320
 Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
 325 330 335
 Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
 340 345 350
 Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
 355 360 365
 Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
 370 375 380
 Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
 385 390 395 400
 Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
 405 410 415
 Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
 420 425 430
 Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
 435 440 445
 Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
 450 455 460
 Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
 465 470 475 480
 Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
 485 490 495
 Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
 500 505 510
 Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
 515 520 525
 Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
 530 535 540
 Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
 545 550 555 560
 Thr Gln Glu Asn Lys Ala Lys Ser
 565

<210> 10
 <211> 568
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

<400> 10
 Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1 5 10 15

Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
		35					40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50					55					60				
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr
65					70					75					80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
				85					90					95	
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
			100					105					110		
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
		115					120					125			
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
	130					135					140				
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145					150					155					160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
				165					170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195					200					205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225					230					235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275					280					285			
Thr	Glu	Phe	Gln	Lys	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325					330					335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385					390					395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
			405						410					415	
Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		
Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val
		435					440					445			

Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
450						455					460				
Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
465					470					475					480
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser
				485					490					495	
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys
			500					505					510		
Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser
		515					520					525			
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn
530						535					540				
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn
545					550					555					560
Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser								
				565											

<210> 11
 <211> 565
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

<400> 11

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
		35					40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr
50					55						60				
Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile
65				70					75						80
Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp
			85						90					95	
Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys
			100				105						110		
Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys
		115					120					125			
Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly
130						135					140				
Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp
145				150					155						160
Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr
			165						170					175	
Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile
			180					185					190		
Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr
		195					200					205			
Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys
210						215						220			

Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	
225					230				235						240	
Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	
				245					250					255		
Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	
			260					265					270			
Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	
		275					280					285				
Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	
	290					295					300					
Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	
305					310				315						320	
Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	
				325					330					335		
Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	
			340					345					350			
Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	
		355					360					365				
Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	
	370					375					380					
Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	
385					390					395					400	
His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	
				405					410					415		
Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	
			420					425					430			
Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	
		435					440					445				
Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser	
	450					455					460					
Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr	
465					470					475					480	
Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	
				485					490					495		
Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	
			500					505					510			
Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Ser	Ser	
		515					520					525				
Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	
	530					535					540					
Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	
545					550					555					560	
Asn	Lys	Ala	Lys	Ser												
				565												

<210> 12
 <211> 566
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

<400> 12

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
		35					40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50					55					60				
Lys	Glu	Thr	Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr
65					70					75					80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
				85					90				95		
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
			100					105					110		
Glu	Met	Lys	Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
		115					120					125			
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
	130					135					140				
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145					150					155					160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
				165					170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195					200					205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215						220			
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225					230					235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275					280					285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295						300			
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325					330					335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385					390					395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
				405					410					415	
Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		

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Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
    435          440          445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
    450          455          460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465          470          475          480
Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
    485          490          495
Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro
    500          505          510
Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly
    515          520          525
Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys
    530          535          540
Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln
545          550          555          560
Glu Asn Lys Ala Lys Ser
    565

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<210> 13
<211> 568
<212> PRT
<213> Artificial Sequence

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<220>
<223> ORF0657nH

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<400> 13
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1          5          10          15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
    20          25          30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
    35          40          45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
    50          55          60
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
65          70          75          80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
    85          90          95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
    100          105          110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
    115          120          125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
    130          135          140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145          150          155          160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
    165          170          175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
    180          185          190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
    195          200          205

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Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
210						215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225					230					235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275					280					285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325					330					335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385					390					395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
			405					410						415	
Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		
Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val
		435					440					445			
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
	450					455					460				
Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
465					470					475					480
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Lys	Val	Glu	Ser	Ser
				485				490					495		
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys
			500					505					510		
Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser
		515					520					525			
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn
	530					535					540				
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn
545					550					555					560
Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser								
				565											

<210> 14
 <211> 568
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

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<400> 14
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
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Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
      20      25      30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
      35      40      45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
      50      55      60
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
65      70      75      80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Glu
      85      90      95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
      100      105      110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
      115      120      125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
      130      135      140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145      150      155      160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Ala Ser Tyr Asp Thr Val
      165      170      175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Ile Ser Asn Gly Thr Lys Ala
      180      185      190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
      195      200      205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
      210      215      220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
225      230      235      240
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
      245      250      255
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
      260      265      270
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
      275      280      285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
      290      295      300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
305      310      315      320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
      325      330      335
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
      340      345      350
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
      355      360      365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
      370      375      380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385      390      395      400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
      405      410      415

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Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		
Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val
		435					440					445			
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
	450					455					460				
Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
465					470					475					480
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser
			485						490						495
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Val	Lys
			500					505					510		
Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser
		515					520					525			
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn
	530					535					540				
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn
545					550					555					560
Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser								
			565												

<210> 15
 <211> 564
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

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Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1 5 10 15
Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
20 25 30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
35 40 45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Ala Pro Lys Glu Thr
50 55 60
Lys Ala Val Lys Pro Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile
65 70 75 80
Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp
85 90 95
Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys
100 105 110
Lys Glu Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys
115 120 125
Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly
130 135 140
Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp
145 150 155 160
Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr
165 170 175
Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile
180 185 190

Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr
		195					200					205			
Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys
	210					215					220				
Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys
225					230					235					240
Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp
				245					250					255	
Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp
			260					265					270		
Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe
		275					280					285			
Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr
	290					295					300				
Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp
305					310				315						320
Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys
				325					330					335	
Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met
			340					345					350		
Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn
		355					360					365			
Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp
	370					375					380				
Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr
385					390					395					400
His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp
				405					410					415	
Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala
			420					425					430		
Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu
		435					440					445			
Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser
	450					455					460				
Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr
465					470				475						480
Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr
				485					490					495	
Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Ala
			500					505					510		
Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Ser	Ser	Ser
		515					520					525			
Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr
	530					535					540				
Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn
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Lys	Ala	Lys	Ser												

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<220>

<223> ORF0657nH

<400> 16

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Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys	20	25	30	
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	35	40	45	
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr	50	55	60	
Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	65	70	75	80
Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	85	90	95	
Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	100	105	110	
Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	115	120	125	
Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	130	135	140	
Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	145	150	155	160
Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	165	170	175	
Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	180	185	190	
Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	195	200	205	
Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	210	215	220	
Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	225	230	235	240
Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	245	250	255	
Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	260	265	270	
Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	275	280	285	
Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	290	295	300	
Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	305	310	315	320
Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	325	330	335	
Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	340	345	350	
Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	355	360	365	
Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	370	375	380	
Ala	Ile	Val	Arg	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	385	390	395	400
His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp				

				405					410					415			
Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala		
			420					425					430				
Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu		
		435					440					445					
Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser		
450						455				460							
Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr		
465				470					475						480		
Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr		
			485					490						495			
Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr		
			500					505					510				
Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser		
		515					520					525					
Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn		
530						535					540						
Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu		
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Asn	Lys	Ala	Lys	Ser													
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Ala	Leu	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Thr	Lys		
			20					25					30				
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro		
		35					40					45					
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro		
50					55						60						
Lys	Glu	Thr	Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr		
65				70					75						80		
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala		
			85					90					95				
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe		
		100					105					110					
Glu	Met	Lys	Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser		
	115						120					125					
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile		
130						135				140							
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr		
145				150					155						160		
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val		
			165						170					175			

Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	180	185	190
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	195	200	205
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	210	215	220
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	225	230	235
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	245	250	255
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	260	265	270
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	275	280	285
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	290	295	300
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	305	310	315
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	325	330	335
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	340	345	350
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	355	360	365
Ile	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	370	375	380
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	385	390	395
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	405	410	415
Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	420	425	430
Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	435	440	445
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	450	455	460
Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	465	470	475
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	485	490	495
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	500	505	510
Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	515	520	525
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	530	535	540
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	545	550	555
Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser									565		

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<220>

<223> ORF0657nH

<400> 18

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Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys	20	25	30	
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	35	40	45	
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr	50	55	60	
Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	65	70	75	80
Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	85	90	95	
Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	100	105	110	
Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	115	120	125	
Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	130	135	140	
Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	145	150	155	160
Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	165	170	175	
Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	180	185	190	
Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	195	200	205	
Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	210	215	220	
Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	225	230	235	240
Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	245	250	255	
Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	260	265	270	
Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	275	280	285	
Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	290	295	300	
Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	305	310	315	320
Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	325	330	335	
Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	340	345	350	
Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	355	360	365	
Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	370	375	380	

Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr
385					390					395					400
His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp
				405					410					415	
Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala
			420					425					430		
Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu
		435					440					445			
Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Pro	Leu	Pro	Ser
	450					455					460				
Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr
465					470					475					480
Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr
				485					490					495	
Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr
			500					505					510		
Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Ser	Ser
		515					520					525			
Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn
	530					535					540				
Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu
545					550					555					560
Asn	Lys	Ala	Lys	Ser											
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Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
		35					40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50					55					60				
Lys	Glu	Thr	Lys	Ala	Val	Lys	Pro	Ala	Thr	Lys	Ala	Asp	Asn	Asn	Thr
65				70						75					80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
				85					90					95	
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
			100					105					110		
Glu	Met	Lys	Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
		115					120					125			
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
	130					135						140			
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145					150					155					160

Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	
				165					170					175		
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	
			180					185					190			
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	
		195					200					205				
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	
	210					215					220					
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	
225					230					235					240	
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	
				245					250					255		
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	
			260					265					270			
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	
		275					280					285				
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	
	290					295					300					
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	
305					310					315					320	
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	
				325					330					335		
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	
			340					345					350			
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	
		355					360					365				
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	
	370					375					380					
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	
385					390					395					400	
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	
			405						410					415		
Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	
			420					425					430			
Arg	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	
		435					440					445				
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	
	450					455					460					
Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	
465					470					475					480	
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	
				485					490					495		
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	
			500					505					510			
Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	
		515					520					525				
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	
	530					535					540					
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	
545					550					555					560	
Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser									
				565												

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Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	1	5	10	15
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys	20	25	30	
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	35	40	45	
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	50	55	60	
Lys	Glu	Thr	Lys	Ala	Val	Lys	Pro	Ala	Thr	Lys	Ala	Asp	Asn	Asn	Thr	65	70	75	80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	85	90	95	
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	100	105	110	
Glu	Met	Lys	Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	115	120	125	
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	130	135	140	
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	145	150	155	160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	165	170	175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	180	185	190	
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	195	200	205	
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	210	215	220	
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	225	230	235	240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	245	250	255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	260	265	270	
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	275	280	285	
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	290	295	300	
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	305	310	315	320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	325	330	335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	340	345	350	
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	355	360	365	

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Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
 370          375          380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
 385          390          395          400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
          405          410          415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
          420          425          430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
          435          440          445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
 450          455          460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
 465          470          475          480
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
          485          490          495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
          500          505          510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
          515          520          525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
 530          535          540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
 545          550          555          560
Thr Gln Glu Asn Lys Ala Lys Ser
          565

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<210> 21
<211> 576
<212> PRT
<213> Artificial Sequence

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<220>
<223> ORF0657nH

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<400> 21
Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1          5          10          15
Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
          20          25          30
Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys
          35          40          45
Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys
 50          55          60
Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro
 65          70          75          80
Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu
          85          90          95
Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala
          100          105          110
Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr
          115          120          125
Gln Gln Phe Tyr His Tyr Ala Gly Ser Val Lys Pro Ala Arg Val Ile
 130          135          140

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Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln
145					150					155					160
Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile
				165					170						175
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe
			180					185					190		
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His
		195					200					205			
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala
	210					215					220				
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr
225				230					235						240
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu
			245						250					255	
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys
		260						265					270		
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu
		275					280					285			
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro
	290					295					300				
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr
305					310					315					320
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His
			325						330					335	
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu
			340					345					350		
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg
		355					360					365			
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile
	370					375					380				
Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val
385					390					395					400
His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val
			405						410					415	
Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Ala	Asp	Lys	Thr	Asn	Lys	Lys
			420					425					430		
Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Thr	Thr	Pro	Ala	Met	Pro
		435					440					445			
Ser	Lys	Pro	Thr	Thr	Pro	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp
	450				455						460				
Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Ser	Pro	Gly	Val	Glu	Lys	Glu	Asn
465					470					475					480
Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Met	Pro	Val	Thr	Lys	Pro
			485						490					495	
Ala	Lys	Ala	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val
			500					505					510		
Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Glu	Thr
		515					520					525			
Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp
	530					535					540				
Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His
545					550					555					560
Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser
			565						570					575	

<210> 22
 <211> 576
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

<400> 22
 Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
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 Ala Val Ala Ser Pro Thr Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
 20 25 30
 Lys Pro Val Ala Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys
 35 40 45
 Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys
 50 55 60
 Ala Val Lys Glu Val Lys Ala Pro Lys Glu Ala Lys Glu Glu Lys Pro
 65 70 75 80
 Ala Ala Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu
 85 90 95
 Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala
 100 105 110
 Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr
 115 120 125
 Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile
 130 135 140
 Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln
 145 150 155 160
 Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile
 165 170 175
 Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe
 180 185 190
 Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His
 195 200 205
 Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala
 210 215 220
 Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr
 225 230 235 240
 Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu
 245 250 255
 Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys
 260 265 270
 Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu
 275 280 285
 Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro
 290 295 300
 Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr
 305 310 315 320
 Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His
 325 330 335
 Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu
 340 345 350

Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg
		355					360					365			
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile
	370					375					380				
Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val
385					390					395					400
His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val
				405					410					415	
Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Ala	Asp	Lys	Thr	Asn	Lys	Lys
			420					425					430		
Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Thr	Thr	Pro	Ala	Met	Pro
		435					440					445			
Ser	Lys	Pro	Thr	Thr	Pro	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp
	450					455					460				
Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Ser	Pro	Ser	Val	Glu	Lys	Glu	Asn
465					470					475					480
Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Met	Pro	Val	Thr	Lys	Pro
				485					490					495	
Ala	Lys	Ala	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val
			500					505					510		
Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Glu	Thr
		515					520					525			
Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp
	530					535					540				
Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His
545					550					555					560
Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser
				565					570					575	

<210> 23
 <211> 568
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

<400> 23

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Ser	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
			35				40					45			
Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50					55					60				
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Thr	Lys	Ala	Asp	Asn	Asn	Thr
65					70					75					80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
				85					90				95		
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
			100				105						110		
Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
		115					120					125			

Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
130						135					140				
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145					150					155					160
Glu	Gly	Asn	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
				165					170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195					200					205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Gly
	210					215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ser	Pro
225					230					235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275					280					285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325					330					335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385					390					395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
			405					410						415	
Asn	Ala	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		
Lys	Glu	Thr	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Thr	Pro	Pro	Val
		435					440					445			
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
	450					455					460				
Ser	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
465					470					475					480
Asp	Lys	Thr	Pro	Thr	Thr	Lys	Pro	Ala	Lys	Ala	Glu	Val	Glu	Ser	Ser
				485				490						495	
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys
			500					505					510		
Pro	Thr	Thr	Ala	Ser	Ser	Glu	Thr	Thr	Ile	Asp	Val	Val	Gln	Thr	Ser
		515					520					525			
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn
	530					535					540				
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Glu	Asn	Asn	Lys	Asn
545					550					555					560

Thr Gln Glu Asn Lys Ala Lys Ser
565

<210> 24
<211> 568
<212> PRT
<213> Artificial Sequence

<220>
<223> ORF0657nH

<400> 24
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
1 5 10 15
Ala Val Ala Ser Pro Ser Thr Thr Thr Glu Lys Ala Pro Glu Ala Lys
20 25 30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
35 40 45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50 55 60
Lys Glu Thr Lys Glu Val Lys Pro Ala Thr Lys Ala Asp Asn Asn Thr
65 70 75 80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
85 90 95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
100 105 110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
115 120 125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130 135 140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145 150 155 160
Glu Gly Asn Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
165 170 175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
180 185 190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
195 200 205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
210 215 220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ser Pro
225 230 235 240
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
245 250 255
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
260 265 270
Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
275 280 285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
290 295 300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
305 310 315 320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
325 330 335

Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385					390					395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
			405					410						415	
Asn	Ala	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		
Lys	Glu	Thr	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Thr	Pro	Pro	Val
		435					440					445			
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
	450					455					460				
Ser	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
465					470					475					480
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Ala	Glu	Val	Glu	Ser	Ser
			485					490						495	
Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys
			500					505					510		
Pro	Thr	Thr	Ala	Ser	Ser	Glu	Thr	Thr	Ile	Asp	Val	Val	Gln	Thr	Ser
		515					520						525		
Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn
	530					535					540				
Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Glu	Asn	Asn	Lys	Asn
545					550					555					560
Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser								
				565											

<210> 25
 <211> 568
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

<400> 25															
Ala	Glu	Glu	Thr	Gly	Gly	Thr	Ile	Thr	Glu	Thr	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala	Lys
			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Ala	Ala	Pro
			35				40					45			
Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50					55					60				
Asn	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ser	Asp	Asn	Asn	Thr
65					70					75					80
Tyr	Pro	Ile	Leu	Asn	Glu	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
			85						90				95		
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
			100					105					110		

Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
		115					120					125			
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
	130					135					140				
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145					150					155					160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
				165					170					175	
Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
		195					200					205			
Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225					230					235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275						280				285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325					330					335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Glu	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375				380					
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385					390					395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
				405					410					415	
Asn	Ala	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		
Lys	Glu	Thr	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Thr	Ala	Pro	Val
		435					440					445			
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
	450					455					460				
Ser	Pro	Ser	Val	Glu	Lys										

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 545 550 555 560
 Thr Gln Glu Asn Lys Ala Lys Ser
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<210> 26
 <211> 568
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

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 Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Val Ala Pro
 35 40 45
 Thr Thr Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
 50 55 60
 Asn Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ser Asp Asn Asn Thr
 65 70 75 80
 Tyr Pro Ile Leu Asn Glu Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
 85 90 95
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
 100 105 110
 Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
 115 120 125
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
 130 135 140
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
 145 150 155 160
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
 165 170 175
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
 180 185 190
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
 195 200 205
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
 210 215 220
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
 225 230 235 240
 Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
 245 250 255
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
 260 265 270
 Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
 275 280 285
 Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
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 Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
 305 310 315 320

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Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
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Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
      340      345      350
Asp Phe Met Val Glu Gly Glu Arg Val Arg Thr Ile Ser Lys Asp Ala
      355      360      365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
      370      375      380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385      390      395      400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
      405      410      415
Asn Ala Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
      420      425      430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Thr Ala Pro Val
      435      440      445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
      450      455      460
Ser Pro Ser Val Glu Lys Glu Ile Asp Ala Ser Ser Glu Ser Gly Lys
465      470      475      480
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
      485      490      495
Ser Thr Thr Pro Thr Lys Val Val Ser Ala Thr Gln Asn Val Ala Lys
      500      505      510
Pro Thr Ser Ala Ser Ser Glu Thr Thr Lys Gly Val Val Gln Thr Ser
      515      520      525
Ala Gly Ser Ser Glu Ala Lys Asp Asn Ala Pro Leu Gln Lys Ala Asn
      530      535      540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
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Thr Gln Glu Asn Lys Ala Lys Ser
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<210> 27
<211> 570
<212> PRT
<213> Artificial Sequence

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<220>
<223> ORF0657nH

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<400> 27
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Thr Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu
      20      25      30
Thr Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu
      35      40      45
Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys
      50      55      60
Ala Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn
65      70      75      80
Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn
      85      90      95

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Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	
			100					105					110			
Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	
		115					120					125				
Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	
	130					135					140					
Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	
145					150					155					160	
Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	
				165					170						175	
Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	
			180					185					190			
Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	
		195					200					205				
Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	
	210					215					220					
Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	
225					230					235					240	
Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	
				245					250					255		
Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	
			260					265					270			
Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	
		275					280					285				
Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	
	290					295					300					
Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	
305					310					315					320	
Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	
				325					330					335		
Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	
			340					345					350			
Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	
		355					360						365			
Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	
	370					375					380					
Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	
385					390					395					400	
Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	
				405					410					415		
Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	
			420					425					430			
Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	
		435					440					445				
Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	
	450					455					460					
Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	
465					470					475					480	
Gly	Lys	Gly	Val	Thr	Leu	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	
				485					490					495		
Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	
			500					505					510			
Ala	Lys	Pro	Thr	Thr	Gly	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	
		515					520					525				

Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys
530						535				540					
Ala	Asn	Ile	Lys	His	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn
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Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser						
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<210> 28
 <211> 654
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SEQ ID NO: 2 modified to contain a glycine after
 the amino terminus methionine and a carboxyl
 His-Tag

<400> 28

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Lys	Ser	Ser	Leu	Gly	Val	Ala	Ser	Val	Ala	Ile	Ser	Thr	Leu	Leu	Leu
			20					25					30		
Leu	Met	Ser	Asn	Gly	Glu	Ala	Gln	Ala	Ala	Ala	Glu	Glu	Thr	Gly	Gly
		35					40					45			
Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	Ala	Val	Ala	Ser	Pro	Thr
	50					55					60				
Thr	Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys	Pro	Val	Ala	Asn	Ala	Val
65					70					75					80
Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	Thr	Ser	Glu	Thr	Lys	Glu
			85						90					95	
Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr	Lys	Glu	Val
			100					105					110		
Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln
		115					120					125			
Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His
	130					135					140				
Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp
145					150					155					160
Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg
			165						170					175	
Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser
			180					185					190		
Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu
		195					200					205			
Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile
	210					215					220				
Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser
225					230					235					240
Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu
			245						250					255	
Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu
		260						265					270		
Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr
		275					280					285			

Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro
290						295					300				
Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys
305					310					315					320
Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val
				325					330					335	
Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val
			340					345					350		
Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val
		355					360					365			
Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val
	370					375					380				
Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly
385					390					395					400
Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr
				405					410					415	
Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val
			420					425					430		
Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg
		435					440					445			
Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn
	450					455					460				
Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala
465					470					475					480
Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys
				485					490					495	
Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys
			500					505					510		
Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr
		515					520					525			
Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys
	530					535					540				
Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser
545					550					555					560
Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala
				565					570					575	
Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp
			580					585					590		
Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala
		595					600					605			
Lys	Ser	Leu	Pro	Gln	Thr	Gly	Glu	Glu	Ser	Asn	Lys	Asp	Met	Thr	Leu
	610					615					620				
Pro	Leu	Met	Ala	Leu	Leu	Ala	Leu	Ser	Ser	Ile	Val	Ala	Phe	Val	Leu
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Pro	Arg	Lys	Arg	Lys	Asn	Leu	Glu	His	His	His	His	His	His		
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<210> 29

<211> 1962

<212> DNA

<213> Artificial Sequence

<220>

<223> Full length ORF0657n + Carboxyl His-Tag

<400> 29

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<210> 30

<211> 1737

<212> DNA

<213> Artificial Sequence

<220>

<223> ORF0657nH + Carboxyl His-Tag

<400> 30

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gacaaagatc atagcgcacc aaactctcgt ccaattgatt ttgaaatgaa aaagaaagat 360
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gattcaaaac cagaaattga attaggatta caatcaggtc aatttttgag aaaatttgaa 480
gtttatgaag gtgacaaaaa gttgccaatt aaattagtat catacgatac tgttaaagat 540
tatgcttaca ttcgcttctc tgtatcaaac ggaacaaaag ctgttaaaat tgtagttca 600

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gcgccatata aaaaagcgaa aacactagaa agacaagttt atgaattaaa taaaattcaa 780
gataaacttc ctgaaaaatt aaaggctgag tacaagaaga aattagagga taaaagaaa 840
gcttttagatg agcaagtga atcagctatt actgaattcc aaaatgtaca accaacaat 900
gaaaaaatga ctgattttaca agatacaaaa tatgtttgtt atgaaagtgt tgagaataac 960
gaatctatga tggatacttt tgttaaacac cctattaaaa caggtatgct taacggcaaa 1020
aaatatatgg tcatggaaac tactaatgac gattactgga aagatttcat ggttgaagg 1080
caacgtgtta gaactataag caaagatgct aaaaataata ctagaacaat tattttccca 1140
tatgttgaag gtaaaactct atatgatgct atcgttaaag ttcacgtaaa aacgattgat 1200
tatgatggac aataccatgt cagaatcggt gataaagaag catttcaaaa agccaatacc 1260
gataaatcta acaaaaaaga acaacaagat aactcagcta agaaggaagc tactccagct 1320
acgcctagca aaccaacacc atcacctggt gaaaaagaat cacaaaaaca agacagccaa 1380
aaagatgaca ataaacaatt accaagtgtt gaaaaagaaa atgacgcata tagtgagtca 1440
ggtaaagaca aaacgcctgc taaaaaacca actaaagggt aagtagaatc aagtagtaca 1500
actccaacta aggtagtatc tacgactcaa aatgttgcaa aaccaacaac tgcttcatca 1560
aaaacaacaa aagatgttgt tcaaacttca gcagggtcta gcgaagcaaa agatagtgtc 1620
ccattacaaa aagcaaacat taaaaacaca aatgatggac acactcaaag ccaaaacaat 1680
aaaaatacac aagaaaataa agcaaaatca ctcgagcacc accaccacca ccactga 1737

```

<210> 31

<211> 1941

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 28 without a carboxyl His-Tag
and is codon optimized for yeast expression

<400> 31

```

atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60
ggtgttgctt ctgtcgctat ctccaccttg ttgttggtga tgtctaacgg tgaagctcaa 120
gctgctgctg aagaaactgg tggtaccaac actgaagctc aaccaagac cgaagctgtc 180
gcttcccaaa ccactacctc tgaaaaggct ccagaaacta agccagttgc taacgctgtc 240
tccgtttcta acaaggaagt cgaagctcca acctccgaaa ctaaggaagc taaggaagtt 300
aaggaagtca aggctccaaa ggaaactaag gaagtcaagc cagctgctaa ggctaccaac 360
aacacttacc caattttgaa ccaagaattg agagaagcta ttaagaacct agctatcaag 420
gacaaggacc actccgctcc aaactctaga ccaatcgact tcgaaatgaa gaagaaggac 480
ggtacccaac aattctacca ctacgcgtcc tctgtcaagc cagctagagt tattttcacc 540
gactctaagc cagaaatcga attgggtttg caatccggtc aattctggag aaagttcgaa 600
gtctacgaag gtgacaagaa gttgccaaat aagttggttt cctacgacac cgtcaaggac 660
tacgcttaca tcagattctc cgtttctaac ggtactaagg ctgtcaagat tgtctcttcc 720
accacttca acaacaagga agaaaagtac gactacactt tgatggaatt cgctcaacca 780
atttacaact ctgctgacaa gttcaagacc gaagaagact acaaggctga aaagttgttg 840
gctccataca agaaggctaa gactttggaa agacaagttt acgaattgaa caagatccaa 900
gacaagttgc cagaaaagtt gaaggctgaa tacaagaaga agttggaaga caccaagaag 960
gctttggacg aacaagtcaa gtccgctatc accgaattcc aaaacgttca accaactaac 1020
gaaaagatga ctgacttgca agacactaag tacgtcgtct acgaatccgt cgaaaacaac 1080
gaatccatga tggacacctt cgtaagcac ccaattaaga ctggtatgtt gaacggtaag 1140
aagtacatgg tcatggaaac cactaacgac gactactgga aggacttcat ggttgaagg 1200
caaagagtca gaaccatctc caaggacgct aagaacaaca ctagaaccat tatcttccca 1260
tacgttgaag gtaagacttt gtacgacgct atcgtaagg ttcacgtaaa gactattgac 1320
tacgacggtc aataccacgt tagaattgtt gacaaggaag ctttcaccaa ggctaaccac 1380
gacaagtcca acaagaagga acaacaagac aactctgcta agaaggaagc taccacagct 1440
accccatcta agccaacccc atctccagtt gaaaaggaat ctcaaaagca agactcccaa 1500

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aaggacgaca acaagcaatt gccatccgtc gaaaaggaaa acgacgcgtc ttctgaatcc 1560
ggtaaggaca agactccagc taccaagcca actaagggtg aagttgaatc ttcctctact 1620
actccaacca aggttgtctc cactacccaa aacgtcgcta agccaactac cgcttcttcc 1680
aagactacca aggacgttgt ccaaacttct gctggttcct ctgaagctaa ggactctgct 1740
ccattgcaaa aggctaacat caagaacacc aacgacggtc acaccaatc ccaaaacaac 1800
aagaacactc aagaaaacaa ggctaagtct ttgccacaaa ccggtgaaga atccaacaag 1860
gacatgacct tgccattgat ggctttgttg gctttgtctt ccacgttgc tttcgtcttg 1920
ccaagaaaga gaaagaacta a

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<210> 32

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 3 and is codon optimized for yeast expression

<400> 32

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgctcctt gtcaagccag cttagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaatataa ttggtttctt acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccga attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtc tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccactctcaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctgtctt tgaatccggt 1440
aaggacaaga ctccagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa

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<210> 33

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 1 and is codon optimized for yeast expression

<400> 33

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaatatag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggatttcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccctctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccata a                                     1341

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<210> 34

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus methionine and is codon optimized for yeast expression

<400> 34

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaatatag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggatttcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960

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tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggg tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggg 1440
aaggggtgtca ctttgggtac caagccaact aaggggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

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<210> 35

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus
methionine and is codon optimized for yeast
expression

<400> 35

```

atgggtgaag aaactgggtg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggg 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagtatt tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttctt acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggg actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggg tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggg 1440
aagggcggtca ctttgggtac caagccaact aaggggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

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<210> 36
 <211> 1710
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encodes SEQ ID NO: 7 containing an amino terminus
 methionine and is codon optimized for yeast
 expression

<400> 36
 atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
 tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
 gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
 gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
 acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300
 aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
 acccaacaat tctaccacta cgcgctcctc gtcaagccag ctagagttag tttcaccgac 420
 tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
 tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
 gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
 cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
 tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
 ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
 aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
 ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
 aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
 tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
 tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
 agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
 gttgaaggta agactttgta cgacgctatc gtcaagggttc acgtcaagac tattgactac 1200
 gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
 aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
 ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1380
 gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
 aagggtgtta ctttgggtac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
 ccaaccaagg ttgtctccac tacccaaaaac gtcgctaagc caactaccgg ttcttccaag 1560
 actaccaagg acgttggtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
 ttgcaaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
 aacactcaag aaaacaaggc taagtcttaa 1710

<210> 37
 <211> 1710
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encodes SEQ ID NO: 7 containing an amino terminus
 methionine and is codon optimized for yeast
 expression

<400> 37
 atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
 tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
 gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180

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gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgctcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatataa ttgggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatggtgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggttc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattggtgac aagggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcga aaggaaaacg acgctcttc tgaatccggt 1440
aagggcggtta ctttggttac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca ccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

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<210> 38

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus
methionine and is codon optimized for yeast
expression

<400> 38

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atgggtgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgtc 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgctcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatataa ttgggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatggtgaa cggtaagaag 1020

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tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattggtgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgctcga aaggaaaacg acgcgtcttc tgaatccggt 1440
aagggtgtca ctttagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttggtcca aacttctgct gggtcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

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<210> 39

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus
methionine and is codon optimized for yeast
expression

<400> 39

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atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgtc 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcca agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
accaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttaa ttccaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatataa ttggtttctt acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tggaaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattggtgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgctcga aaggaaaacg acgcgtcttc tgaatccggt 1440
aagggtgtca ctttggctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ctcttccaag 1560
actaccaagg acgttggtcca aacttctgct gggtcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

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<210> 40

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus
methionine and is codon optimized for yeast
expression

<400> 40

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atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
accaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttaa ttccaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggtggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtagaag 1020
tacatggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattggttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac ccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aagggtgtta ctttagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgg ttcttccaag 1560
actaccaagg acgttggtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa

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<210> 41

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 7 containing an amino terminus
methionine and is codon optimized for yeast
expression

<400> 41

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atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240

```

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acttacccaa ttttgaacca agaattgaga gaagctatta agaaccacgc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttag tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac ttgggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtt acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctgtctt tgaatccggt 1440
aagggtgtta ctttgggtac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaaac gtcgctaagc caactaccgg ctcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaaagg ctaacatcaa gcacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

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<210> 42

<211> 481

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nI+

<400> 42

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Met Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr
 1          5          10          15
Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr
          20          25          30
Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala
          35          40          45
Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala
          50          55          60
Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn
65          70          75          80
Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro
          85          90          95
Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp
          100          105          110
Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala
          115          120          125
Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu
          130          135          140
Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val
145          150          155          160

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Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	
				165					170					175		
Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	
			180					185					190			
Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	
		195					200					205				
Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	
	210					215					220					
Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	
225					230					235					240	
Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	
				245					250					255		
Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	
			260					265					270			
Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	
		275					280					285				
Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	
	290				295						300					
Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	
305					310					315					320	
Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	
				325					330					335		
Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	
			340					345					350			
Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	
		355					360					365				
Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	
	370					375					380					
Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	
385					390					395					400	
Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	
				405					410					415		
Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	
			420					425					430			
Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	
		435					440					445				
Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	
	450					455					460					
Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	
465					470					475					480	
Lys																

<210> 43

<211> 1452

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 42 and is codon optimized for yeast expression

<400> 43

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60

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tccccaacca ctacctctga aaagggtcca gaaactaage cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
accaacaat tctaccacta cgcgctcctct gtcaagccag ctagagttag tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatataa ttgggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattggtgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aagtaaggat cc 1452

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<210> 44
 <211> 605
 <212> PRT
 <213> ORF0657nG

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<400> 44
Met Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr
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Glu Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr
          20          25          30
Lys Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala
          35          40          45
Pro Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala
          50          55          60
Pro Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn
          65          70          75          80
Thr Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro
          85          90          95
Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp
          100          105          110
Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala
          115          120          125
Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu
          130          135          140
Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val
          145          150          155          160
Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr
          165          170          175
Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys
          180          185          190

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Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys
		195					200					205			
Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala
	210					215					220				
Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala
225					230					235					240
Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn
				245					250					255	
Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys
			260					265					270		
Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala
		275					280					285			
Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp
	290					295					300				
Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu
305					310					315					320
Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu
				325					330					335	
Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp
			340					345					350		
Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp
		355					360					365			
Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys
	370					375					380				
Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr
385					390					395					400
Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys
				405					410					415	
Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala
			420					425					430		
Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro
		435					440					445			
Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys
	450					455					460				
Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly
465					470					475					480
Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser
				485					490					495	
Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala
			500					505					510		
Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr
		515					520					525			
Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala
	530					535					540				
Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys
545					550					555					560
Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser	Leu	Pro	Gln	Thr	Gly	Glu	Glu
				565					570					575	
Ser	Asn	Lys	Asp	Met	Thr	Leu	Pro	Leu	Met	Ala	Leu	Leu	Ala	Leu	Ser
			580					585					590		
Ser	Ile	Val	Ala	Phe	Val	Leu	Pro	Arg	Lys	Arg	Lys	Asn			
		595					600					605			

<210> 45

<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 44 containing an amino terminus
methionine and is codon optimized for yeast
expression

<400> 45

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggaa gtcaagccag ctgctaaggc taccaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa gaaggacggt 360
acccaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat ctcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacggttag aattggttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aaggacaaga ctccagctac caagccaact aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttggtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatcca aaacaacaag 1680
aacactcaag aaaacaaggc taagtctttg ccacaaaccg gtgaagaatc caacaaggac 1740
atgaccttgc cattgatggc tttgttggtt ttgtcttcca tcgttgcttt cgtcttgcca 1800
agaaagagaa agaactaa                                     1818

```

<210> 46

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 17 containing an amino terminus
methionine and is codon optimized for yeast
expression

<400> 46

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agcttttggt 60
tccccaacca ctaccactga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120

```

```

gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatatag ttgggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagttttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccactctcaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattggtgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1440
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttgtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1620
ttgcaaaaagg ctaacatcaa gaacaccaac gacgggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

<210> 47

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes the SEQ ID NO: 17 I+ region, is codon optimized for yeast expression, and encodes a methionine initiation codon

<400> 47

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttgggt 60
tccccaacca ctaccactga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatatag ttgggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagttttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960

```

```

tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggg tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aagtaa                                           1446

```

<210> 48
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encodes the SEQ ID NO: 17 I region, is codon
 optimized for yeast expression, and encodes a
 methionine initiation codon

```

<400> 48
atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttggct 60
tccccaacca ctaccactga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgctcctc gtcaagccag ctagagttaa tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccgggtcaat tctggagaaa gttcgaagtc 480
tacgaagggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggg tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacgggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccata a                                           1341

```

<210> 49
 <211> 1938
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encodes for full length ORF0657n containing SEQ ID
 NO: 17 modified to contain a glycine after the
 amino terminus methionine and is codon optimized
 for yeast expression

<400> 49

```

atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60
ggtgttgctt ctgtcgctat ctccaccttg ttgttggtga tgtctaacgg tgaagctcaa 120
gctgctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctttggct 180
tccccaacca ctaccactga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 240
gtttctaaca aggaagtcca agctccaacc tccgaaacta aggaagctaa ggaagttaag 300
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctgctaaggc tgacaacaac 360
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 420
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 480
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 540
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 600
tacgaagggtg acaagaagtt gccaatataag ttggtttcct acgacaccgt caaggactac 660
gcttacatca gattctccgt ttctaaccgt actaaggctg tcaagattgt ctcttcacc 720
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 780
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 840
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 900
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 960
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 1020
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 1080
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1140
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggt tgaaggctcaa 1200
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1260
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1320
gacggtcaat accacgttag aattggtgac aaggaagctt tcaccaaggc taacaccgac 1380
aagttccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1440
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaaag 1500
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgctcttc tgaatccggt 1560
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1620
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1680
actaccaagg acgttggtcca aacttctgct ggttcctctg aagctaagga ctctgctcca 1740
ttgcaaaaagg ctaacatcaa gaacaccaac gacggtcaca ccaatccca aaacaacaag 1800
aacactcaag aaaacaaggc taagtctttg ccacaaaccg gtgaagaatc caacaaggac 1860
atgaccttgc cattgatggc tttgttggtt ttgtcttcca tcgttgcttt cgtcttgcca 1920
agaaagagaa agaactaa

```

<210> 50

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 20, is codon optimized for yeast expression, and encodes a methionine initiation codon

<400> 50

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtcca agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480

```

```

tacgaaggtg acaagaagtt gccaatlaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggg tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac ccagctacc 1320
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcga aaggaaaacg acgctcttc tgaatccggt 1440
aaggacaaga ctccagctac caagccagct aagggtgaag ttgaatcttc ctctactact 1500
ccaaccaagg ttgtctccac tacccaaaac gtcgctaagc caactaccgc ttcttccaag 1560
actaccaagg acgttggtcca aacttctgct gggtcctctg aagctaagga ctctgctcca 1620
ttgcaaaagg ctaacatcaa gaacaccaac gacggtcaca cccaatccca aaacaacaag 1680
aacactcaag aaaacaaggc taagtcttaa 1710

```

<210> 51

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes SEQ ID NO: 20 I+ region, is codon
optimized for yeast expression, and encodes a
methionine initiation codon

<400> 51

```

atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaagggtcca gaaactaagc cagttgctaa cgctgtctcc 120
gttttctaaca aggaagtcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctcaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagttat tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaatlaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttccacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcgc tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttgttggct 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtca tggaaaccac taacgacgac tactggaagg acttcatggg tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacgttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagtccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac ccagctacc 1320

```

```
ccatctaagc caaccccatc tccagttgaa aaggaatctc aaaagcaaga ctcccaaaag 1380
gacgacaaca agcaattgcc atccgtcgaa aaggaaaacg acgcgtcttc tgaatccggt 1440
aagtaa 1446
```

<210> 52
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encodes the SEQ ID NO: 20 I region, is codon optimized for yeast expression, and encodes a methionine initiation codon

```
<400> 52
atggctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 60
tccccaacca ctacctctga aaaggctcca gaaactaagc cagttgctaa cgctgtctcc 120
gtttctaaca aggaagtgcga agctccaacc tccgaaacta aggaagctaa ggaagttaag 180
gaagtcaagg ctccaaagga aactaaggct gtcaagccag ctactaaggc tgacaacaac 240
acttacccaa ttttgaacca agaattgaga gaagctatta agaaccagc tatcaaggac 300
aaggaccact ccgctccaaa ctctagacca atcgacttcg aaatgaagaa ggaaaacggt 360
gaacaacaat tctaccacta cgcgtcctct gtcaagccag ctagagtatt tttcaccgac 420
tctaagccag aaatcgaatt gggtttgcaa tccggtcaat tctggagaaa gttcgaagtc 480
tacgaaggtg acaagaagtt gccaatgaag ttggtttcct acgacaccgt caaggactac 540
gcttacatca gattctccgt ttctaacggt actaaggctg tcaagattgt ctcttcacc 600
cacttcaaca acaaggaaga aaagtacgac tacactttga tgggaattcg tcaaccaatt 660
tacaactctg ctgacaagtt caagaccgaa gaagactaca aggctgaaaa gttggttggt 720
ccatacaaga aggctaagac tttggaaaga caagtttacg aattgaacaa gatccaagac 780
aagttgccag aaaagttgaa ggctgaatac aagaagaagt tgggaagacac caagaaggct 840
ttggacgaac aagtcaagtc cgctatcacc gaattccaaa acgttcaacc aactaacgaa 900
aagatgactg acttgcaaga cactaagtac gtcgtctacg aatccgtcga aaacaacgaa 960
tccatgatgg acaccttcgt taagcaccca attaagactg gtatgttgaa cggtaagaag 1020
tacatgggtc tggaaaccac taacgacgac tactggaagg acttcatggt tgaagggtcaa 1080
agagtcagaa ccatctccaa ggacgctaag aacaacacta gaaccattat cttcccatac 1140
gttgaaggta agactttgta cgacgctatc gtcaagggtc acgtcaagac tattgactac 1200
gacggtcaat accacggttag aattgttgac aaggaagctt tcaccaaggc taacaccgac 1260
aagccaaca agaaggaaca acaagacaac tctgctaaga aggaagctac cccagctacc 1320
ccatctaagc caaccccata a 1341
```

<210> 53
 <211> 1938
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encodes for full length ORF0657n containing SEQ ID NO: 20 modified to contain a glycine after the amino terminus methionine and is codon optimized for yeast expression

```
<400> 53
atgggtaaca agcaacaaaa ggaattcaag tctttctact ccattagaaa gtcttccttg 60
gggtgttgct ctgtcgctat ctccaccttg ttgttggtga tgtctaacgg tgaagctcaa 120
gctgctgaag aaactggtgg taccaacact gaagctcaac caaagaccga agctgtcgct 180
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Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
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Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr
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Lys	Ala	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile
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Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp
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Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys
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Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys
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Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly
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Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr
				165					170					175	
Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile
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Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys
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Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe
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Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr
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Lys	Tyr	Ala	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp
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Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys
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Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met
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Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn
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Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp
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Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr
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His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp
				405					410					415	
Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala
			420					425					430		
Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu
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Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser
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Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr
465					470					475					480
Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr
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Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr
			500					505					510		
Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Ser	Ser
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Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn
	530					535					540				
Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu
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<213> Artificial Sequence

<220>
<223> ORF0657nH

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35 40 45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50 55 60
Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
65 70 75 80
Tyr Pro Ile Leu Asn Gln Gly Leu Arg Glu Ala Ile Lys Asn Pro Ala
85 90 95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
100 105 110
Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
115 120 125
Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
130 135 140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145 150 155 160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
165 170 175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
180 185 190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
195 200 205
Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
210 215 220
Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
225 230 235 240
Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys
245 250 255
Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
260 265 270
Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Pro Ala Ile
275 280 285
Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
290 295 300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
305 310 315 320
Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
325 330 335

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Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
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Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
	370					375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385					390					395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
			405					410						415	
Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		
Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val
		435					440					445			
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Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
465					470				475						480
Asp	Lys	Thr	Pro	Ala	Thr	Lys	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser
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Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys
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Pro	Ile	Thr	Ala	Ser	Ser	Lys	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser
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Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn
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Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn
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			20					25					30		
Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro
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Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro
	50					55					60				
Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr
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Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Glu
				85					90				95		
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
			100					105					110		

Glu 115	Met 130	Lys 115	Lys 130	Lys 150	Asp 135	Gly 150	Thr 120	Gln 135	Gln 155	Phe 140	Tyr 125	His 125	Tyr 145	Ala 160	Ser 175
Ser 145	Val 160	Lys 135	Pro 150	Ala 170	Arg 140	Val 135	Ile 120	Phe 155	Thr 140	Asp 125	Ser 125	Lys 145	Pro 160	Glu 175	Ile 190
Glu 165	Leu 180	Gly 140	Leu 165	Gln 180	Ser 160	Gly 170	Gln 145	Phe 170	Trp 160	Arg 145	Lys 130	Phe 150	Glu 175	Val 190	Tyr 205
Glu 180	Gly 195	Asp 160	Lys 180	Lys 200	Leu 185	Pro 170	Ile 150	Lys 185	Leu 170	Val 155	Ser 135	Tyr 150	Asp 175	Thr 190	Val 205
Lys 200	Asp 215	Tyr 185	Ala 200	Tyr 220	Ile 205	Arg 190	Phe 175	Ser 200	Ile 185	Ser 160	Asn 140	Gly 155	Thr 175	Lys 190	Ala 205
Val 215	Lys 230	Ile 200	Val 215	Ser 230	Ser 210	Thr 200	His 180	Phe 210	Asn 190	Asn 170	Lys 150	Glu 165	Glu 190	Lys 205	Tyr 220
Asp 230	Tyr 245	Thr 210	Leu 230	Met 245	Glu 220	Phe 215	Ala 195	Gln 225	Pro 200	Ile 180	Tyr 160	Asn 175	Ser 200	Ala 215	Asp 230
Lys 245	Phe 260	Lys 225	Thr 245	Glu 260	Glu 240	Asp 225	Tyr 235	Lys 250	Ala 220	Glu 200	Lys 180	Leu 205	Leu 230	Ala 245	Pro 260
Tyr 260	Lys 275	Lys 250	Ala 260	Lys 280	Thr 265	Leu 250	Glu 240	Arg 265	Gln 230	Val 210	Tyr 190	Glu 215	Leu 240	Asn 265	Lys 280
Ile 275	Gln 290	Asp 265	Lys 280	Leu 300	Pro 270	Glu 255	Lys 245	Leu 280	Lys 255	Ala 230	Glu 215	Tyr 235	Lys 260	Lys 285	Lys 300
Leu 290	Glu 305	Asp 280	Thr 305	Lys 320	Lys 300	Ala 285	Leu 260	Asp 300	Glu 270	Gln 250	Val 230	Lys 245	Ser 270	Ala 295	Ile 310
Thr 305	Glu 320	Phe 300	Gln 315	Asn 330	Val 310	Gln 300	Pro 275	Thr 310	Asn 290	Glu 265	Lys 240	Met 260	Thr 290	Asp 315	Leu 330
Gln 320	Asp 335	Thr 310	Lys 325	Tyr 340	Val 320	Val 310	Tyr 290	Glu 320	Ser 300	Val 275	Glu 250	Asn 270	Asn 300	Glu 325	Ser 340
Met 335	Met 350	Asp 325	Thr 340	Phe 350	Val 330	Lys 320	His 300	Pro 325	Ile 300	Lys 280	Thr 255	Gly 275	Met 300	Leu 335	Asn 350
Gly 350	Lys 365	Lys 340	Tyr 365	Met 370	Val 350	Met 340	Glu 310	Thr 350	Thr 325	Asn 290	Asp 265	Asp 285	Tyr 310	Trp 335	Lys 350
Asp 365	Phe 380	Met 355	Val 370	Glu 380	Gly 360	Gln 350	Arg 320	Val 370	Arg 340	Thr 310	Ile 280	Ser 295	Lys 320	Asp 345	Ala 360
Lys 380	Asn 395	Asn 370	Thr 380	Arg 390	Thr 370	Ile 360	Ile 330	Phe 380	Pro 350	Tyr 320	Val 290	Glu 305	Gly 330	Lys 355	Thr 370
Leu 395	Tyr 410	Asp 380	Ala 400	Ile 410	Val 380	Lys 370	Val 340	His 390	Val 360	Lys 330	Thr 300	Ile 315	Asp 340	Tyr 365	Asp 380
Gly 410	Gln 425	Tyr 390	His 415	Val 420	Arg 395	Ile 380	Val 350	Asp 400	Lys 370	Glu 340	Ala 310	Phe 325	Thr 350	Lys 375	Ala 390
Asn 425	Thr 440	Asp 405	Lys 420	Ser 430	Asn 400	Lys 390	Lys 360	Glu 410	Gln 380	Gln 350	Asp 320	Asn 335	Ser 360	Ala 385	Lys 405
Lys 440	Glu 455	Ala 410	Thr 440	Pro 450	Ala 420	Thr 410	Pro 370	Ser 420	Lys 390	Pro 360	Thr 330	Pro 345	Ser 370	Pro 390	Val 415
Glu 455	Lys 470	Glu 420	Ser 450	Gln 460	Lys 430	Gln 420	Asp 380	Ser 430	Gln 400	Lys 370	Asp 340	Asp 355	Asn 380	Lys 400	Gln 420
Leu 470	Pro 485	Ser 430	Val 460	Glu 470	Lys 440	Glu 430	Asn 390	Asp 440	Ala 410	Ser 380	Ser 350	Glu 365	Ser 390	Gly 410	Lys 430
Asp 485	Lys 500	Thr 440	Pro 470	Ala 480	Thr 450	Lys 440	Pro 400	Ala 450	Lys 420	Gly 390	Glu 360	Val 375	Glu 400	Ser 420	Ser 440
Ser 500	Thr 515	Thr 450	Pro 480	Thr 490	Lys 460	Val 450</									

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 Thr Gln Glu Asn Lys Ala Lys Ser
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 35 40 45
 Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
 50 55 60
 Lys Glu Thr Lys Glu Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
 65 70 75 80
 Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Thr Lys Asn Pro Glu
 85 90 95
 Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Thr Asp Phe
 100 105 110
 Glu Met Lys Lys Asn Asp Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser
 115 120 125
 Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
 130 135 140
 Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
 145 150 155 160
 Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
 165 170 175
 Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Ile Ser Asn Gly Thr Lys Ala
 180 185 190
 Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Tyr
 195 200 205
 Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp
 210 215 220
 Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro
 225 230 235 240
 Tyr Lys Lys Ala Lys Thr Xaa Glu Arg Gln Val Tyr Glu Leu Asn Lys
 245 250 255
 Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys
 260 265 270

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Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile
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Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu
    290                                295                300
Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser
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Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn
    325                                330                335
Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys
    340                                345                350
Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala
    355                                360                365
Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr
    370                                375                380
Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp
385                                390                395                400
Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala
    405                                410                415
Asn Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys
    420                                425                430
Lys Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val
    435                                440                445
Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln
    450                                455                460
Leu Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys
465                                470                475                480
Asp Lys Thr Pro Ala Thr Lys Pro Ala Lys Gly Glu Val Glu Ser Ser
    485                                490                495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
    500                                505                510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
    515                                520                525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
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<212> PRT

<213> Artificial Sequence

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<223> ORF0657nH

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Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
    35                                40                45

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Lys	Glu	Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr
65					70					75					80
Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala
				85					90					95	
Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe
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Glu	Met	Lys	Lys	Glu	Asn	Gly	Thr	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser
		115					120					125			
Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile
	130					135					140				
Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr
145					150					155					160
Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val
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Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala
			180					185					190		
Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr
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Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp
	210					215					220				
Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro
225					230					235					240
Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys
				245					250					255	
Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys
			260					265					270		
Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile
		275					280					285			
Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu
	290					295					300				
Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser
305					310					315					320
Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn
				325					330					335	
Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys
			340					345					350		
Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala
		355					360					365			
Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr
						375					380				
Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp
385					390					395					400
Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala
				405					410					415	
Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys
			420					425					430		
Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val
		435					440					445			
Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln
	450					455					460				
Leu	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys
465					470					475					480

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Asp Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser
      485                      490                      495
Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys
      500                      505                      510
Pro Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser
      515                      520                      525
Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn
      530                      535                      540
Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn
545                      550                      555                      560
Thr Gln Glu Asn Lys Ala Lys Ser
      565

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<210> 59
<211> 567
<212> PRT
<213> Artificial Sequence

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<220>
<223> ORF0657nH

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<400> 59
Ala Glu Glu Thr Gly Gly Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1      5      10      15
Ala Val Ala Ser Pro Thr Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys
      20      25      30
Pro Val Ala Asn Ala Val Ser Val Ser Asn Lys Glu Val Glu Ala Pro
      35      40      45
Thr Ser Glu Thr Lys Glu Ala Lys Glu Val Lys Glu Val Lys Ala Pro
50      55      60
Lys Glu Thr Lys Ala Val Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr
65      70      75      80
Tyr Pro Ile Leu Asn Gln Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala
      85      90      95
Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe
      100     105     110
Glu Met Asn Lys Lys Asn Gly Glu Gln Gln Phe Tyr His Tyr Ala Ser
      115     120     125
Ser Ala Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro Glu Ile
      130     135     140
Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr
145     150     155     160
Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp Thr Val
      165     170     175
Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr Lys Ala
      180     185     190
Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu Lys Asp
      195     200     205
Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys
210     215     220
Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr
225     230     235     240
Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile
      245     250     255

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Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu
      260      265      270
Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr
      275      280      285
Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln
      290      295      300
Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met
305      310      315      320
Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly
      325      330      335
Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp
      340      345      350
Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys
      355      360      365
Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu
      370      375      380
Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly
385      390      395      400
Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn
      405      410      415
Thr Asp Lys Ser Asn Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys
      420      425      430
Glu Ala Thr Pro Ala Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu
      435      440      445
Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu
      450      455      460
Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp
465      470      475      480
Lys Thr Pro Ala Thr Lys Pro Thr Lys Gly Glu Val Glu Ser Ser Ser
      485      490      495
Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro
      500      505      510
Thr Thr Ala Ser Ser Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala
      515      520      525
Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile
      530      535      540
Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr
545      550      555      560
Gln Glu Asn Lys Ala Lys Ser
      565

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<210> 60

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> ORF0657nH

<400> 60

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Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1      5      10      15
Ala Val Ala Ser Pro Thr Thr Thr Thr Glu Lys Ala Pro Glu Ala
      20      25      30

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Lys	Pro	Val	Ala	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys
		35					40					45			
Glu	Val	Val	Ala	Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys
	50					55					60				
Ala	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Ala	Lys	Glu	Glu	Lys	Pro
65					70					75					80
Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu
				85					90					95	
Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala
			100					105					110		
Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr
		115					120					125			
Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile
	130					135					140				
Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln
145					150					155					160
Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile
				165					170					175	
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe
			180					185					190		
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His
		195					200					205			
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala
	210					215					220				
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr
225					230					235					240
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu
				245					250					255	
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys
			260					265					270		
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu
		275					280					285			
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro
	290					295					300				
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Ala	Tyr
305					310					315					320
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His
				325					330					335	
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu
			340					345					350		
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg
		355					360					365			
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile
	370					375					380				
Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val
385					390					395					400
His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val
				405					410					415	
Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Ala	Asp	Lys	Thr	Asn	Lys	Lys
			420					425					430		
Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Thr	Thr	Pro	Ala	Met	Pro
		435					440					445			
Ser	Lys	Pro	Thr	Thr	Pro	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp
	450					455					460				

Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Ser	Pro	Ser	Val	Glu	Lys	Glu	Asn
465					470					475					480
Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Met	Pro	Val	Thr	Lys	Pro
				485					490					495	
Ala	Lys	Ala	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val
			500					505					510		
Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Glu	Thr
		515					520					525			
Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp
	530					535					540				
Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His
545					550					555					560
Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser
				565					570					575	

<210> 61
 <211> 572
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

<400> 61

Ala	Glu	Glu	Thr	Gly	Val	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala
			20					25					30		
Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Val	Ala
		35				40						45			
Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Val	Lys	Glu
	50				55						60				
Val	Lys	Ala	Pro	Lys	Glu	Ala	Lys	Glu	Glu	Lys	Pro	Ala	Ala	Lys	Ala
65				70					75						80
Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile
			85					90					95		
Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg
			100					105					110		
Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr
		115				120						125			
His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser
	130				135						140				
Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys
145				150					155						160
Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser
			165					170						175	
Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn
		180						185					190		
Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys
		195				200						205			
Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr
	210					215					220				
Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys
225				230						235					240

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Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr
      245      250      255
Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu
      260      265      270
Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu Asp Glu Gln Val
      275      280      285
Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys
      290      295      300
Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu
305      310      315      320
Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr
      325      330      335
Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp
      340      345      350
Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile
      355      360      365
Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Cys Val
      370      375      380
Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr
385      390      395      400
Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val Asp Lys Glu Ala
      405      410      415
Phe Thr Lys Ala Asn Ala Asp Lys Thr Asn Lys Lys Glu Gln Gln Asp
      420      425      430
Asn Ser Ala Lys Lys Glu Thr Thr Pro Ala Met Pro Ser Lys Pro Thr
      435      440      445
Thr Pro Pro Val Glu Lys Glu Ser Gln Lys Gln Asp Ser Gln Lys Asp
      450      455      460
Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Asn Asp Ala Ser Ser
465      470      475      480
Glu Ser Gly Lys Asp Lys Met Pro Val Thr Lys Pro Ala Lys Ala Glu
      485      490      495
Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val Ser Thr Thr Gln
      500      505      510
Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Glu Thr Thr Lys Asp Val
      515      520      525
Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser Ala Pro Leu
      530      535      540
Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His Thr Gln Ser Gln
545      550      555      560
Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
      565      570

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<210> 62
<211> 572
<212> PRT
<213> Artificial Sequence

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<220>
<223> ORF0657nH

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<400> 62
Ala Glu Glu Thr Gly Val Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu
 1           5           10           15

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Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala
			20					25					30		
Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Val	Ala
		35					40					45			
Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Val	Lys	Glu
	50				55						60				
Val	Lys	Ala	Pro	Lys	Glu	Ala	Lys	Glu	Glu	Lys	Pro	Ala	Ala	Lys	Ala
65				70						75					80
Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu	Arg	Glu	Ala	Ile
			85						90				95		
Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg
			100					105					110		
Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Lys	Asp	Gly	Thr	Gln	Gln	Phe	Tyr
		115					120					125			
His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser
	130					135					140				
Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys
145					150					155					160
Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser
				165					170					175	
Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn
			180					185					190		
Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys
		195					200					205			
Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr
	210					215					220				
Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys
225					230					235					240
Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr
				245					250					255	
Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu
			260					265					270		
Tyr	Lys	Lys	Lys	Leu	Glu	Glu	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val
		275					280					285			
Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys
	290					295					300				
Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu
305					310					315					320
Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr
				325					330					335	
Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp
			340					345					350		
Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile
		355					360					365			
Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Val
	370					375					380				
Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr
385					390					395					400
Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala
				405					410					415	
Phe	Thr	Lys	Ala	Asn	Ala	Asp	Lys	Thr	Asn	Lys	Lys	Glu	Gln	Gln	Asp
			420					425					430		
Asn	Ser	Ala	Lys	Lys	Glu	Thr	Thr	Pro	Ala	Met	Pro	Ser	Lys	Pro	Thr
		435					440					445			

Thr	Pro	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp
450						455					460				
Asp	Asn	Lys	Gln	Ser	Pro	Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser
465					470					475					480
Glu	Ser	Gly	Lys	Asp	Lys	Met	Pro	Val	Thr	Lys	Pro	Ala	Lys	Ala	Glu
				485					490					495	
Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln
			500					505					510		
Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Glu	Thr	Thr	Lys	Asp	Val
		515					520					525			
Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu
	530					535					540				
Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln
545					550					555					560
Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser				
				565					570						

<210> 63
 <211> 566
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ORF0657nH

<400> 63

Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu
1				5					10					15	
Ala	Val	Ala	Ser	Pro	Thr	Thr	Thr	Thr	Thr	Glu	Lys	Ala	Pro	Glu	Ala
			20					25					30		
Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val	Ser	Asn	Lys	Glu	Val	Val	Ala
		35					40					45			
Pro	Thr	Thr	Glu	Thr	Lys	Glu	Ala	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu
	50					55					60				
Thr	Lys	Glu	Val	Lys	Pro	Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro
65				70					75						80
Ile	Leu	Asn	Lys	Glu	Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys
			85						90					95	
Asp	Lys	Asp	His	Ser	Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met
			100					105					110		
Lys	Lys	Glu	Asn	Gly	Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val
		115					120					125			
Lys	Pro	Ala	Arg	Val	Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu
	130					135						140			
Gly	Leu	Gln	Ser	Gly	Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly
145					150					155					160
Asp	Lys	Lys	Leu	Pro	Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp
			165						170					175	
Tyr	Ala	Tyr	Ile	Arg	Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys
			180					185					190		
Ile	Val	Ser	Ser	Thr	His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr
		195					200					205			
Thr	Leu	Met	Glu	Phe	Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe
	210					215						220			

Lys	Thr	Glu	Glu	Asp	Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	225	230	235	240
Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	245	250	255	
Asp	Lys	Leu	Pro	Glu	Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	260	265	270	
Glu	Thr	Lys	Lys	Ala	Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	275	280	285	
Phe	Gln	Asn	Val	Gln	Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	290	295	300	
Thr	Lys	Tyr	Val	Val	Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	305	310	315	320
Asp	Thr	Phe	Val	Lys	His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	325	330	335	
Lys	Tyr	Met	Val	Met	Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	340	345	350	
Met	Val	Glu	Gly	Gln	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	355	360	365	
Asn	Thr	Arg	Thr	Ile	Ile	Phe	Pro	Tyr	Ile	Glu	Gly	Lys	Thr	Leu	Tyr	370	375	380	
Asp	Ala	Ile	Val	Lys	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	385	390	395	400
Tyr	His	Val	Arg	Ile	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Ala	405	410	415	
Asp	Lys	Ser	Asn	Lys	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	420	425	430	
Thr	Thr	Pro	Ala	Thr	Pro	Ser	Lys	Pro	Thr	Thr	Pro	Pro	Val	Glu	Lys	435	440	445	
Glu	Ser	Gln	Lys	Gln	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Thr	Gln	Ser	Pro	450	455	460	
Ser	Val	Glu	Lys	Glu	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	465	470	475	480
Thr	Pro	Ala	Thr	Lys	Pro	Ala	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	485	490	495	
Thr	Pro	Thr	Lys	Val	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	500	505	510	
Thr	Ala	Ser	Ser	Glu	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	515	520	525	
Pro	Ser	Glu	Ala	Lys	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	530	535	540	
Asn	Thr	Asn	Asp	Gly	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	545	550	555	560
Glu	Asp	Lys	Ala	Lys	Ser											565			

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<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> His-Tag

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<220>
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<210> 66
<211> 17
<212> DNA
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<220>
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<400> 66
caggaaacag ctatgac 17

<210> 67
<211> 39
<212> DNA
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<220>
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<400> 67
aaccggtttt ccatggggaa caaacagcaa aaagaattt 39

<210> 68
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<212> DNA
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<400> 68
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 ggtggttgctt ctgtcgctat ctccaccttg ttggtggtga tgtctaacg 109

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<210> 73
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<210> 76
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<210> 79
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<220>
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<400> 79
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 aaagacaagt ttacgaattg aacaagatcc aagacaagtt gccaga 106

<210> 80
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<220>
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<400> 81
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 gactgacttg caagacacta agtacgtcgt ctacgaatcc gtcgaaaac 109

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<220>
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<400> 82
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<400> 83

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<210> 84

<211> 101

<212> DNA

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<400> 84

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<210> 85

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<212> DNA

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<210> 87

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<210> 89
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<400> 90
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<400> 92

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<212> DNA

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<210> 94

<211> 31

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<213> Artificial Sequence

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<223> Primer

<400> 94

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<210> 95

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 95

tgataagctt gctcaatggc tctcttcctc 30

<210> 96

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 96

aaccggtttg gatcccacaa aacaaaatgg gtaacaagca acaaaaggaa ttc 53

<210> 97

<211> 42

<212> DNA

<213> Artificial Sequence

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<210> 98
<211> 24
<212> DNA
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<400> 98
gctgaagaaa ctggtggtac caac 24

<210> 99
<211> 42
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<212> DNA
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<210> 101
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<400> 101
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<211> 32

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<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

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39

<210> 105

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 105

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38

<210> 106

<211> 644

<212> PRT

<213> S. aureus

<400> 106

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			20					25					30		
Met	Ser	Asn	Gly	Glu	Ala	Gln	Ala	Ala	Glu	Glu	Thr	Gly	Gly	Thr	Asn
		35					40					45			
Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	Ala	Leu	Ala	Ser	Pro	Thr	Thr	Thr
	50					55					60				

Thr	Glu	Lys	Ala	Pro	Glu	Thr	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser	Val
65					70					75					80
Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala	Lys
				85					90					95	
Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr	Lys	Ala	Val	Lys	Pro
			100					105					110		
Ala	Ala	Lys	Ala	Asp	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu	Leu
		115					120					125			
Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser	Ala
	130					135					140				
Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Glu	Asn	Gly	Glu
145					150					155					160
Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val	Ile
				165					170					175	
Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	Gln
			180					185					190		
Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Ile
		195					200					205			
Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe
	210					215					220				
Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His
225					230					235					240
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala
				245					250					255	
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr
			260					265					270		
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu
		275					280					285			
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys
	290					295					300				
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu
305					310					315					320
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro
				325					330					335	
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr
			340					345					350		
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His
		355					360					365			
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu
	370					375						380			
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg
385					390					395					400
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Ile	Asn	Asn	Thr	Arg	Thr	Ile	Ile
				405					410					415	
Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val
			420					425					430		
His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val
		435					440					445			
Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys
	450					455					460				
Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro
465					470					475					480
Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp
				485					490					495	

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Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu Asn
500 505 510
Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys Pro
515 520 525
Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val
530 535 540
Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys Thr
545 550 555 560
Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp
565 570 575
Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His
580 585 590
Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
595 600 605
Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro Leu
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Lys Arg Lys Asn

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<210> 107
<211> 644
<212> PRT
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35 40 45
Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr
50 55 60
Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser Val
65 70 75 80
Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys
85 90 95
Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Ala Val Lys Pro
100 105 110
Ala Thr Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu
115 120 125
Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala
130 135 140
Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Glu Asn Gly Glu
145 150 155 160
Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile
165 170 175
Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln
180 185 190
Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile
195 200 205

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Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe
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Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	His
225					230					235					240
Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe	Ala
				245					250					255	
Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp	Tyr
			260					265					270		
Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu	Glu
		275					280					285			
Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu	Lys
290						295					300				
Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	Leu
305					310					315					320
Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln	Pro
				325					330					335	
Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val	Tyr
			340					345					350		
Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys	His
		355					360					365			
Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met	Glu
370						375					380				
Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	Arg
385					390					395					400
Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	Ile
			405						410					415	
Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys	Val
			420					425					430		
His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile	Val
		435					440					445			
Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys	Lys
450						455				460					
Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	Pro
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Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	Asp
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Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	Asp
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Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly	His
			580					585					590		
Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys	Ser
		595					600					605			
Leu	Pro	Gln	Thr	Gly	Glu	Glu	Ser	Asn	Lys	Asp	Met	Thr	Leu	Pro	Leu
610						615					620				
Met	Ala	Leu	Leu	Ala	Leu	Ser	Ser	Ile	Val	Ala	Phe	Val	Leu	Pro	Arg
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